BEST AVAILABLE COPY

Replacement Sheet

A. IIA1 V_H sequences [NA, SEQ ID NO: 13; AA, SEQ ID NO: 46]



ATGGCTGTCCTGGGGCTGCTTCTCTGCCTGGTGACTTTCCCAAGCTGTGTCCTGTCCCAG $\begin{smallmatrix} M&A&V&L&G&L&L&L&C&L&V&T&F&P&S&C&V&L&S&\mathbf{Q}\end{smallmatrix}$ 61 GTGCAGCTGAAGGAGTCAGGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCCATCACA Q L K E S G P G L V A P S Q S L S I T 121 TGCACCATCTCAGGGTTCTCATTAACCGACTATGGTGTTCACTGGGTTCGCCAGCCTCCA CTISGFSLT DYGVHWVRQPP GGAAAGGGTCTGGAGTGGCTGGTAGTGATTTGGAGTGATGGAAGCTCAACCTATAATTCA 181 G K G L E W L V V I W S D G S S T Y N S 241 GCTCTCAAATCCAGAATGACCATCAGGAAGGACAACTCCAAGAGCCAAGTTTTCTTAATA L K S R M T I R K D N S K S Q V F L I 301 ATGAACAGTCTCCAAACTGATGACTCAGCCATGTACTACTGTGCCAGACATGGAACTTAC M N S L Q T D D S A M Y Y C A R H G T Y TACGGTATGACTACGACGGGGGATGCTTTGGACTACTGGGGTCAAGGAACCTCAGTCACC 361 Y G M T T T G D A L D Y W G Q G T S V T 421 GTCTCCTCA V S S

B. IIA1 V_L sequences [NA, SEQ ID NO: 47]

 ${f ATGGATTTTCAGGTGCAGATTTTCAGCTTCCTGCTAATCAGTGCCTCAGTCATAATGTCC}$ M D F Q V Q I F S F L L I S A S V I M S AGAGGACAAATTGTTCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCTAGGGGAACGG R G Q I V L T Q S P A I M S A S L G E R 121 GTCACCATGACCTGCACTGCCAGTTCAAGTGTAAGTTCCAATTACTTGCACTGGTACCAG VTMTCTASS SVSSNYLHWYQ CAGAAGCCAGGATCCGCCCCAATCTCTGGATTTATAGCACATCCAACCTGGCTTCTGGA 181 WIYSTSNLASG QKPGSAPNL GTCCCAGCTCGTTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGC 241 V P A R F S G S G S G T S Y S L T I S S ATGGAGGCTGAAGATGCTGCCACTTATTACTGCCACCAGTATCTTCGTTCCCCACCGACG 301 MEAEDAATYYCHQYLRSPPT 361 TTCGGTGGAGGCACCAAGCTGGAAATCAAA FGGGTKLEIK

FIGURE 3